ABSTRACT

The present invention provides an approach for developing an algorithm for determining the effectiveness of anti-viral drugs based on a comprehensive analysis of paired phenotypic and genotypic data guided by phenotypic clinical cut-offs. In one aspect, the algorithm allows one to provide a patient with effective treatment. It helps predict whether an infected individual will respond to treatment with an anti-viral compound, thereby allowing an effective treatment regimen to be designed without subjecting the patient to unnecessary side effects. Also, by avoiding the administration of ineffective drugs, considerable time and money is saved.